

















































Related Structures

| Sequences producing significant alignments: | | | Score (bits) | E Value | |
|--|--|---------------------|-----------------|-------------------|--|
| gi 6912284 ref NP_036245.1 | carbonic anhydrase XIV precurso... | 682 | 0.0 | L | |
| gi 22760422 dbj BAC11191.1 | unnamed protein product [Homo s... | 681 | 0.0 | L | |
| gi 6753264 ref NP_035927.1 | carbonic anhydrase 14; CA XIV [... | 548 | e-155 | L | |
| gi 47168790 pdb 1RJ5 A | Chain A, Crystal Structure Of The Ex... | 438 | e-122 | S | |
| gi 21431756 sp Q9MZ30 CAHC_RABIT | Carbonic anhydrase XII pre... | 270 | 3e-71 | | |
| gi 4502515 ref NP_001209.1 | carbonic anhydrase XII isoform ... | 264 | 2e-69 | L | |
| gi 30585185 gb AAP36865.1 | Homo sapiens carbonic anhydrase ... | 263 | 5e-69 | | |
| gi 45935383 ref NP_996808.1 | carbonic anhydrase XII isoform... | 263 | 5e-69 | L | |
| gi 26342835 dbj BAC35074.1 | unnamed protein product [Mus mu... | 262 | 9e-69 | L | |
| gi 31541884 ref NP_848483.2 | carbonic anyhydrase 12 [Mus mu... | 261 | 1e-68 | L | |
| gi 34864283 ref XP_343417.1 | similar to 2310047E01Rik prote... | 261 | 1e-68 | L | |
| gi 47221597 emb CAF97862.1 | unnamed protein product [Tetrao... | 261 | 2e-68 | | |
| gi 21595173 gb AAH31385.1 | Car12 protein [Mus musculus] | 260 | 3e-68 | L | |
| gi 47225853 emb CAF98333.1 | unnamed protein product [Tetrao... | 254 | 1e-66 | | |
| gi 34858063 ref XP_342298.1 | similar to CA XIV [Rattus norv... | 246 | 4e-64 | L | |
| gi 15826782 pdb 1JCZ A | Chain A, Crystal Structure Of The Ex... | 246 | 6e-64 | S | |
| gi 47211349 emb CAF93821.1 | unnamed protein product [Tetrao... | 240 | 3e-62 | | |
| gi 47228789 emb CAG07521.1 | unnamed protein product [Tetrao... | 236 | 4e-61 | | |
| gi 49117984 gb AAH72918.1 | Unknown (protein for MGC:80389) ... | 209 | 5e-53 | | |
| gi 9955948 ref NP_001207.1 | carbonic anhydrase IX precursor... | 203 | 4e-51 | L | |
| gi 21314850 ref NP_647466.1 | carbonic anhydrase 9 [Mus musc... | 201 | 2e-50 | L | |
| gi 30580354 sp Q8VHB5 CAH9_MOUSE | Carbonic anhydrase IX prec... | 201 | 2e-50 | L | |
| gi 115469 sp P08060 CAH6_SHEEP | Carbonic anhydrase VI (Carbo... | 197 | 2e-49 | | |
| gi 89853 pir A29993 | carbonate dehydratase (EC 4.2.1.1) VI ... | 197 | 4e-49 | | |
| gi 34935135 ref XP_233380.2 | similar to carbonic anhydrase ... | 196 | 5e-49 | L | |
| gi 27806915 ref NP_776323.1 | carbonic anhydrase VI [Bos tau... | 195 | 1e-48 | L | |
| gi 28812184 dbj BAC65098.1 | carbonic anhydrase VI [Canis fa... | 189 | 6e-47 | L | |
| gi 14530767 emb CAC42429.1 | dJ477M7.5 (carbonic anhydrase v... | 186 | 5e-46 | L | |
| gi 1070519 pir CRHU6 | carbonate dehydratase (EC 4.2.1.1) VI... | 184 | 3e-45 | | |
| gi 23503046 sp P23280 CAH6_HUMAN | Carbonic anhydrase VI prec... | 181 | 1e-44 | L | |
| gi 4557397 ref NP_001206.1 | carbonic anhydrase VI precursor... | 181 | 2e-44 | L | |
| gi 31076619 sp Q8UWA5 CAH2_TRIHK | Carbonic anhydrase II (Car... | 180 | 5e-44 | | |
| gi 34872490 ref XP_216584.2 | similar to Car6 protein [Rattu... | 179 | 7e-44 | L | |
| gi 40363537 ref NP_954685.1 | carbonic anhydrase II [Danio r... | 177 | 3e-43 | L | |
| gi 29789369 ref NP_599183.1 | protein tyrosine phosphatase, ... | 176 | 6e-43 | L | |
| gi 25281969 gb AAN72430.1 | receptor-like protein tyrosine p... | 176 | 6e-43 | L | |
| gi 6679559 ref NP_033007.1 | protein tyrosine phosphatase, r... | 176 | 7e-43 | L | |
| gi 25281971 gb AAN72431.1 | receptor-like protein tyrosine p... | 176 | 1e-42 | L | |
| gi 45709528 gb AAH67635.1 | LOC407683 protein [Danio rerio] | 174 | 2e-42 | L | |
| gi 45383516 ref NP_989645.1 | protein tyrosine phosphatase, ... | 174 | 2e-42 | L | |
| gi 18860898 ref NP_002832.2 | protein tyrosine phosphatase, ... | 174 | 3e-42 | L | |
| gi 1263069 gb AAC50439.1 | receptor tyrosine phosphatase gam... | 174 | 3e-42 | L | |
| gi 477137 pir A48148 | protein-tyrosine-phosphatase (EC 3.1.... | 173 | 5e-42 | | |
| gi 25281973 gb AAN72432.1 | receptor-like protein tyrosine p... | 172 | 7e-42 | L | |
| gi 41387130 ref NP_957107.1 | hypothetical protein MGC73385 ... | 172 | 1e-41 | L | |
| gi 29179452 gb AAH49309.1 | Zgc:73385 protein [Danio rerio] | 169 | 1e-40 | L | |
| gi 5921196 sp P18761 CAH6_MOUSE | Carbonic anhydrase VI precu... | 168 | 1e-40 | L | |
| gi 33585712 gb AAH55437.1 | Car6 protein [Mus musculus] | 166 | 9e-40 | L | |
| gi 29612611 gb AAH49973.1 | Car6 protein [Mus musculus] | 166 | 9e-40 | L | |
| gi 50418465 gb AAH78387.1 | Unknown (protein for IMAGE:70369... | 164 | 3e-39 | | |
| gi 34851195 ref XP_226204.2 | similar to carbonic anhydrase ... | 161 | 2e-38 | L | |
| gi 68286 pir CRRB2 | carbonate dehydratase (EC 4.2.1.1) II -... | 161 | 2e-38 | | |

| | | | | |
|---|--|---------------------|-----------------------|---|
| gi 2098445 pdb 1UGF | Human Carbonic Anhydrase Ii [hcai] (...) | 161 | 3e-38 |  |
| gi 28269695 ref NP_444300.1 | carbonic anhydrase 7; carbonic... | 160 | 4e-38 |  |
| gi 47227809 emb CAG08972.1 | unnamed protein product [Tetrao... | 159 | 7e-38 |  |
| gi 4557395 ref NP_000058.1 | carbonic anhydrase II; carbonat... | 159 | 7e-38 |  |
| gi 1942501 pdb 1UGD | Human Carbonic Anhydrase Ii[hcai] (E... | 159 | 7e-38 |  |
| gi 2118910 pir A48993 | protein-tyrosine-phosphatase (EC 3.1... | 159 | 9e-38 |  |
| gi 11513906 pdb 1G3Z A | Chain A, Carbonic Anhydrase Ii (F131... | 159 | 1e-37 |  |
| gi 15080386 gb AAH11949.1 | Carbonic anhydrase II [Homo sapi... | 159 | 1e-37 |  |
| gi 229731 pdb 1CA2 | Carbonic Anhydrase II (Carbonate Dehyd... | 159 | 1e-37 |  |
| gi 442669 pdb 1BCD | Carbonic Anhydrase Ii (E.C.4.2.1.1) Co... | 159 | 1e-37 |  |
| gi 1421269 pdb 1CAN | Carbonic Anhydrase Ii (E.C.4.2.1.1) C... | 159 | 1e-37 |  |
| gi 1942500 pdb 1UGB | Human Carbonic Anhydrase Ii[hcai] (E... | 159 | 1e-37 |  |
| gi 38348436 ref NP_940986.1 | carbonic anhydrase XIII; carbo... | 159 | 1e-37 |  |
| gi 1942499 pdb 1UGA | Human Carbonic Anhydrase Ii[hcai] (E... | 159 | 1e-37 |  |
| gi 2098448 pdb 1UGE | Human Carbonic Anhydrase Ii [hcai] (...) | 159 | 1e-37 |  |
| gi 115448 sp P00917 CAH1_HORSE | Carbonic anhydrase I (Carbon... | 158 | 1e-37 |  |
| gi 22219225 pdb 1LG5 A | Chain A, Crystal Structure Analysis ... | 158 | 1e-37 |  |
| gi 2098447 pdb 1UGC | Human Carbonic Anhydrase Ii [hcai] (...) | 158 | 2e-37 |  |
| gi 22252956 gb AAM94169.1 | erythrocyte carbonic anhydrase [...] | 158 | 2e-37 |  |
| gi 68288 pir CRBO2 | carbonate dehydratase (EC 4.2.1.1) II -... | 158 | 2e-37 |  |
| gi 442701 pdb 1CAJ | Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu... | 158 | 2e-37 |  |
| gi 1065006 pdb 1CNH | Carbonic Anhydrase Ii (Carbonate Dehy... | 158 | 2e-37 |  |
| gi 999629 pdb 1YDB | Carbonic Anhydrase Ii (Carbonate Dehyd... | 158 | 2e-37 |  |
| gi 231119 pdb 5CA2 | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 2e-37 |  |
| gi 1633065 pdb 1ZSC | Carbonic Anhydrase Ii Mutant E117q, H... | 157 | 3e-37 |  |
| gi 442702 pdb 1CAK | Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu... | 157 | 3e-37 |  |
| gi 46048696 ref NP_990648.1 | carbonic anhydrase II [Gallus ...] | 157 | 3e-37 |  |
| gi 231199 pdb 6CA2 | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 3e-37 |  |
| gi 442772 pdb 1CVA | Carbonic Anhydrase Ii (Hca Ii) (E.C.4....) | 157 | 3e-37 |  |
| gi 442826 pdb 1DCA | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 3e-37 |  |
| gi 1065012 pdb 1CNJ | Carbonic Anhydrase Ii (Carbonate Dehy... | 157 | 3e-37 |  |
| gi 1345651 sp P48282 CAH1_SHEEP | Carbonic anhydrase I (Carbo... | 157 | 3e-37 |  |
| gi 229981 pdb 1HED | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 3e-37 |  |
| gi 442703 pdb 1CAL | Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu... | 157 | 3e-37 |  |
| gi 229657 pdb 12CA | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 3e-37 |  |
| gi 1065011 pdb 1CNI | Carbonic Anhydrase Ii (Carbonate Dehy... | 157 | 3e-37 |  |
| gi 999932 pdb 1CCS | Carbonic Anhydrase Ii (Carbonate Dehyd... | 157 | 4e-37 |  |
| gi 1065001 pdb 1CNG | Carbonic Anhydrase Ii (Carbonate Dehy... | 157 | 4e-37 |  |
| gi 442700 pdb 1CAI | Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu... | 157 | 4e-37 |  |
| gi 229978 pdb 1HEA | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 4e-37 |  |
| gi 999632 pdb 1YDD | Carbonic Anhydrase Ii (Carbonate Dehyd... | 157 | 4e-37 |  |
| gi 2554664 pdb 1H9N | H119n Carbonic Anhydrase Ii | 157 | 4e-37 |  |
| gi 2554643 pdb 2H4N | H94n Carbonic Anhydrase Ii Complexed ... | 157 | 4e-37 |  |
| gi 24987658 pdb 1LZV A | Chain A, Site-Specific Mutant (Tyr7 ...) | 157 | 4e-37 |  |
| gi 231320 pdb 9CA2 | Carbonic Anhydrase II (Carbonate Dehyd... | 157 | 4e-37 |  |
| gi 1168741 sp P00919 CAH2_RABIT | Carbonic anhydrase II (Carb... | 157 | 5e-37 |  |
| gi 999935 pdb 1CCT | Carbonic Anhydrase Ii (Carbonate Dehyd... | 156 | 5e-37 |  |
| gi 1289219 emb CAA29417.1 | carbonic anhydrase II [Gallus ga... | 156 | 5e-37 |  |

Alignments

>gi|6912284|ref|NP_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]
 gi|8928036|sp|Q9ULX7|CAHE_HUMAN Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)
 gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]
 gi|21706779|gb|AAH34412.1| Carbonic anhydrase XIV, precursor [Homo sapiens]
 gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]
 Length = 337

Score = 682 bits (1760), Expect = 0.0
 Identities = 337/337 (100%), Positives = 337/337 (100%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120
 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120

Query: 121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
 Sbjct: 121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ 240
 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ
 Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG
 Sbjct: 241 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA 337
 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA 337

>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]
 Length = 337

Score = 681 bits (1756), Expect = 0.0
 Identities = 336/337 (99%), Positives = 336/337 (99%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120
 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120

Query: 121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
 Sbjct: 121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ 240
 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ
 Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG
 Sbjct: 241 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA 337
 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA 337

>gi|6753264|ref|NP_035927.1| carbonic anhydrase 14; CA XIV [Mus musculus]
 gi|8928038|sp|Q9WVT6|CAHE_MOUSE Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV))
 gi|5030908|dbj|BAA78709.1| CA XIV [Mus musculus]
 gi|28422260|gb|AAH46995.1| Carbonic anhydrase 14 [Mus musculus]
 Length = 337

Score = 548 bits (1413), Expect = e-155
 Identities = 283/337 (83%), Positives = 306/337 (90%)

Query: 1 MLFSALLLEVIWILAADGGQHWYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLF ALLL+V WILAADGG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPD
 Sbjct: 1 MLFFALLLKVTWILAADGGHHWTYEGPHGQDHWPTSYPECGGDAQSPINIQTDSVIFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
 LPA+QPHGYDQ GTEPLDLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS G
 Sbjct: 61 LPAVQPHGYDQLGTEPLDLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQRGSLEG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEAT AELH+VHYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS
 Sbjct: 121 SEHQINSEATAAELHVVHYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
 LHE+R+KDQKTSVPPF++REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM Q
 Sbjct: 181 LHEIRYKDQKTSVPPFSVRELFPPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGG 240

Query: 241 LEKLQGTLFSTEEEPKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQ TL STEE+PS+ LVQNYR QPLNQR +FASFIQAG YTTGEML LGVGIL G
 Sbjct: 241 LEKLQETLSSTEEDPSEPLVQNYRVPQPLNQRTIFASFIQAGPLYTTGEMLGLGVGILAG 300

Query: 301 CLCLLLAVYFIARKIRKKRLNRSVVFSAQATTEA 337
 CLCLLLAVYFIA+KIRKKRL NRKSVVFSA+ATTEA
 Sbjct: 301 CLCLLLAVYFIAQKIRKKRLGNRSVVFSAARATTEA 337

>gi|47168790|pdb|1RJ5|A Chain A, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv
 gi|47168791|pdb|1RJ5|B Chain B, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv
 gi|47168792|pdb|1RJ6|A Chain A, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex with Acetazolamide
 gi|47168793|pdb|1RJ6|B Chain B, Crystal Structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex with Acetazolamide
 Length = 261

Score = 438 bits (1127), Expect = e-122
 Identities = 216/261 (82%), Positives = 236/261 (90%)

Query: 18 GGQHWYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLALQPHGYDQPGTEPL 77
 GG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPDLPA+QPHGYDQ GTEPL
 Sbjct: 1 GGHWTYEGPHGQDHWPTSYPECGGDAQSPINIQTDSVIFDPDLPAVQPHGYDQLGTEPL 60

Query: 78 DLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEATFAELHIV 137
 DLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS GSEH INSEAT AELH+V
 Sbjct: 61 DLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQRGSLEGSEHHINSEATAAELHV 120

Query: 138 HYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197
 HYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS LHE+R+KDQKTSVPPF+
 Sbjct: 121 HYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSRLEIRYKDQKTSVPPFS 180

Query: 198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSK 257
 +REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM QLEKLQ TL STEE+PS+
 Sbjct: 181 VRELFPPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGGLEKLQETLSSTEEDPSE 240

Query: 258 LLVQNYRALQPLNQRMFASF 278
 LVQNYR QPLNQR +FASF
 Sbjct: 241 PLVQNYRVPQPLNQRTIFASF 261

Sequences producing significant alignments:

| Sequences producing significant alignments: | | | Score (bits) | E Value | |
|---|---------------------------------------|------|-----------------|------------|--|
| gi 37182499 gb AY358689.1 | Homo sapiens clone DNA62812 CA14... | 3366 | 0.0 | LU | |
| gi 6912283 ref NM_012113.1 | Homo sapiens carbonic anhydrase... | 3350 | 0.0 | LUG | |
| gi 6009639 dbj AB025904.1 | Homo sapiens mRNA for carbonic a... | 3350 | 0.0 | LUG | |
| gi 22760421 dbj AK074765.1 | Homo sapiens cDNA FLJ90284 fis,... | 3313 | 0.0 | LU | |
| gi 21706778 gb BC034412.1 | Homo sapiens carbonic anhydrase ... | 3299 | 0.0 | LUG | |
| gi 19309420 emb AL138795.21 | Human DNA sequence from clone ... | 948 | 0.0 | | |
| gi 28422259 gb BC046995.1 | Mus musculus carbonic anhydrase ... | 805 | 0.0 | LU | |
| gi 6753263 ref NM_011797.1 | Mus musculus carbonic anhydrase... | 805 | 0.0 | LUG | |
| gi 5030907 dbj AB005450.1 | Mus musculus mRNA for CA XIV, co... | 805 | 0.0 | LUG | |
| gi 15384634 emb AL451074.13 | Human DNA sequence from clone ... | 650 | 0.0 | L | |
| gi 12848980 dbj AK012316.1 | Mus musculus 11 days embryo who... | 454 | e-124 | LUG | |
| gi 34858062 ref XM_342297.1 | Rattus norvegicus similar to C... | 373 | e-100 | LU | |
| gi 15082388 gb BC012108.1 | Homo sapiens cDNA clone MGC:2010... | 287 | 4e-74 | LS | |
| gi 26801277 gb AC092855.39 | Mus musculus chromosome 3 clone... | 184 | 4e-43 | | |
| gi 26084135 dbj AK034693.1 | Mus musculus 12 days embryo emb... | 167 | 1e-37 | U | |
| gi 12844826 dbj AK009805.1 | Mus musculus adult male tongue ... | 86 | 3e-13 | LUG | |
| gi 33569140 emb AL845336.9 | Mouse DNA sequence from clone R... | 74 | 1e-09 | | |
| gi 23334838 gb AC123032.5 | Mus musculus BAC clone RP24-480K... | 72 | 4e-09 | | |
| gi 46518694 gb AC125192.3 | Mus musculus BAC clone RP23-266B... | 72 | 4e-09 | | |
| gi 38323102 emb AL954710.27 | Mouse DNA sequence from clone ... | 70 | 2e-08 | | |
| gi 21955088 gb AC122003.2 | Mus musculus BAC clone RP24-336G... | 68 | 7e-08 | | |
| gi 3252819 gb AC004382.1 | HUAC004382 Homo sapiens Chromosome... | 68 | 7e-08 | LS | |
| gi 45476650 gb AC122746.7 | Mus musculus chromosome 17, clon... | 68 | 7e-08 | | |
| gi 4508108 gb AC005101.2 | Homo sapiens BAC clone CTA-352J5 ... | 68 | 7e-08 | L | |
| gi 50355915 gb AC124516.4 | Mus musculus chromosome 12 clone... | 66 | 3e-07 | | |
| gi 50199072 gb AC110559.11 | Mus musculus chromosome 7, clon... | 66 | 3e-07 | | |
| gi 25046688 gb AC112147.5 | Mus musculus BAC clone RP23-175E... | 66 | 3e-07 | | |
| gi 37620322 gb AC111047.9 | Mus musculus chromosome 3, clone... | 66 | 3e-07 | | |
| gi 33590044 gb AC118614.12 | Mus musculus chromosome 18, clo... | 66 | 3e-07 | | |
| gi 29501916 gb AC099600.5 | Mus musculus chromosome 15, clon... | 66 | 3e-07 | | |
| gi 33342291 gb AC126722.7 | Rattus norvegicus 4 BAC CH230-5L... | 66 | 3e-07 | | |
| gi 42475822 emb AL928891.20 | Mouse DNA sequence from clone ... | 66 | 3e-07 | | |
| gi 47131369 gb AC147160.2 | Mus musculus BAC clone RP24-336A... | 66 | 3e-07 | | |
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| gi 15778814 gb AC084382.1 | Mus musculus clone RP23-5K17, co... | 66 | 3e-07 | | |
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| gi 14529749 emb AL138959.20 | Human DNA sequence from clone ... | 66 | 3e-07 | | |
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| gi 41351594 gb AC139938.5 | Mus musculus chromosome 6, clone... | 66 | 3e-07 | | |
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| gi 17646883 gb AC009256.8 | Drosophila melanogaster, chromos... | 64 | 1e-06 | | |
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| gi 33285452 gb AC125123.4 | Mus musculus BAC clone RP24-270C... | 62 | 4e-06 |
| gi 30103094 gb AC122255.2 | Mus musculus BAC clone RP23-178F... | 62 | 4e-06 |
| gi 38424173 gb AC113307.12 | Mus musculus chromosome 3, clon... | 62 | 4e-06 |
| gi 28195584 gb AC124401.3 | Mus musculus BAC clone RP24-362C... | 62 | 4e-06 |
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| gi 37202201 gb AC110573.11 | Mus musculus chromosome 16, clo... | 62 | 4e-06 |
| gi 32813578 gb AC102452.7 | Mus musculus chromosome 5, clone... | 62 | 4e-06 |
| gi 35931637 gb AC109169.13 | Mus musculus chromosome 6, clon... | 62 | 4e-06 |
| gi 32880240 gb AC114559.8 | Mus musculus, clone RP23-50G21, ... | 62 | 4e-06 |
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| gi 46518064 emb BX324154.5 | Zebrafish DNA sequence from clo... | 62 | 4e-06 |
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| gi 47971088 emb AL512589.4 | Mouse DNA sequence from clone R... | 62 | 4e-06 |
| gi 47825293 emb BX511025.10 | Zebrafish DNA sequence from cl... | 62 | 4e-06 |
| gi 46935014 emb BX322574.10 | Zebrafish DNA sequence from cl... | 62 | 4e-06 |
| gi 21728149 dbj AP001531.4 | Homo sapiens genomic DNA, chrom... | 62 | 4e-06 |
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Alignments

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Score = 3366 bits (1698), Expect = 0.0
Identities = 1701/1701 (100%)
Strand = Plus / Plus

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Length = 1757

Score = 3350 bits (1690), Expect = 0.0
Identities = 1698/1701 (99%)
Strand = Plus / Plus

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>gi|6009639|dbj|AB025904.1|  Homo sapiens mRNA for carbonic anhydrase 14, complete cds
Length = 1757

Score = 3350 bits (1690), Expect = 0.0
Identities = 1698/1701 (99%)
Strand = Plus / Plus

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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sbjct: 1540  gaaatcgctgtgttggttaatgcagagaacaaactctgttttagttgcaggggaagtgtgg 1599

Query: 1561  atataccccaagtcctctacccccctcacttttatggccctttccctagatatactgcgg 1620
|||||
sbjct: 1600  atataccccaagtcctctacccccctcacttttatggccctttccctagatatactgcgg 1659

Query: 1621  gatctctccttaggataaagagttgctgttggaagttgtatattttgatcaatatatttg 1680
|||||
sbjct: 1660  gatctctccttaggataaagagttgctgttggaagttgtatattttgatcaatatatttg 1719

Query: 1681  gaaattaaagtttctgacttt 1701
|||||
sbjct: 1720  gaaattaaagtttctgacttt 1740
```

>gi|22760421|dbj|AK074765.1|  Homo sapiens cDNA FLJ90284 fis, clone NT2RP1000613, weakly si
CARBONIC ANHYDRASE VI (EC 4.2.1.1)
Length = 1771

Score = 3313 bits (1671), Expect = 0.0

Identities = 1682/1686 (99%)

Strand = Plus / Plus

```
Query: 1   gagactgcagagggagataaagagagaggggcaaagaggcagcaagagatttgtcctgggg 60
          |||
Sbjct: 86   gagactgcagagggagataaagagagaggggcaaagaggcagcaagagatttgtcctgggg 145

Query: 61   atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 120
          |||
Sbjct: 146  atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 205

Query: 121   gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 180
          |||
Sbjct: 206   gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 265

Query: 181   tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 240
          |||
Sbjct: 266   tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 325

Query: 241   ccagtcccctgcaccccttcttgggacactatgttgttctccgccctcctgctggagggtg 300
          |||
Sbjct: 326   ccagtcccctgcaccccttcttgggacactatgttgttctccgccctcctgctggagggtg 385

Query: 301   atttggatcctggctgcagatgggggtcaacactggacgtatgagggcccatgggtcag 360
          |||
Sbjct: 386   atttggatcctggctgcagatgggggtcaacactggacgtatgagggcccatgggtcag 445

Query: 361   gaccattggccagcctcttaccctgagtggtggaacaatgccagtcgcccacatcgatatt 420
          |||
Sbjct: 446   gaccattggccagcctcttaccctgagtggtggaacaatgccagtcgcccacatcgatatt 505

Query: 421   cagacagacagtgtgacatttgaccctgatttgctgtctgcagccccacggatatgac 480
          |||
Sbjct: 506   cagacagacagtgtgacatttgaccctgatttgctgtctgcagccccacggatatgac 565

Query: 481   cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 540
          |||
Sbjct: 566   cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 625

Query: 541   ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 600
          |||
Sbjct: 626   ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 685

Query: 601   cactgggggtcagaaaggatccccaggggggtcagaacaccagatcaacagtgaagccaca 660
          |||
Sbjct: 686   cactgggggtcagaaaggatccccaggggtcagaacaccagatcaacagtgaagccaca 745


Query: 661   tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 720
          |||
Sbjct: 746   tttgcagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 805
```

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sbjct: 1646 atatacccccagtcctctacccccctcacttttatggccctttccctagatatactgcgg 1705

Query: 1621 gatctctccttaggataaagagttgctgttgaagttgtatatattttgatcaatatatttg 1680
|||||
sbjct: 1706 gatctctccttaggataaagagttgctgttgaagttgtatatattttgatcaatatatttg 1765

Query: 1681 gaaatt 1686
|||||
sbjct: 1766 gaaatt 1771

>gi|21706778|gb|BC034412.1|  Homo sapiens carbonic anhydrase XIV, mRNA (cDNA clone MGC:34
IMAGE:5175251), complete cds
Length = 1767

Score = 3299 bits (1664), Expect = 0.0
Identities = 1669/1671 (99%)
Strand = Plus / Plus

Query: 31 caaagaggcagcaagagatttgcctctggggatccagaaacccatgataccctactgaaca 90
|||||
sbjct: 1 caaagaggcagcaagagatttgcctctggggatccagaaacccatgataccctactgaaca 60

Query: 91 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaatacact 150
|||||
sbjct: 61 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaatacact 120

Query: 151 cagccaggagctcgctcgctctctctctctctctctcactcctccctccctctctctct 210
|||||
sbjct: 121 cagccaggagctcgctcgctctctctctctctctctcactcctccctccctctctctct 180

Query: 211 gcctgtcctagtcctctagtcctcaaattcccagtcaccttgcaccttctctgggacact 270
|||||
sbjct: 181 gcctgtcctagtcctctagtcctcaaattcccagtcaccttgcaccttctctgggacact 240

Query: 271 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 330
|||||
sbjct: 241 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 300

Query: 331 cactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtgt 390
|||||
sbjct: 301 cactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtgt 360

Query: 391 ggaaacaatgccagtcgcccacgatattcagacagacagtggtgacatttgaccctgat 450
|||||
sbjct: 361 ggaaacaatgccagtcgcccacgatattcagacagacagtggtgacatttgaccctgat 420

Query: 451 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagcctttggacctgcac 510
|||||
sbjct: 421 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagcctttggacctgcac 480

Query: 511 aacaatggccacacagtgcaactctctctgcccctctaccctgtatctgggtggacttccc 570
|||||
sbjct: 481 aacaatggccacacagtgcaactctctctgcccctctaccctgtatctgggtggacttccc 540

Query: 571 cgaaaatatgtagctgcccagctccacctgcactgggggtcagaaaggatccccagggggg 630
|||||
sbjct: 541 cgaaaatatgtagctgcccagctccacctgcactgggggtcagaaaggatccccagggggg 600

Query: 631 tcagaacaccagatcaacagtgaagccacatttgagagctccacattgtacattatgac 690
|||
Sbjct: 601 tcagaacaccagatcaacagtgaagccacatttgagagctccacattgtacattatgac 660

Query: 691 tctgattcctatgacagcttgagtgaaggctgctgagaggcctcagggcctggctgtcctg 750
|||
Sbjct: 661 tctgattcctatgacagcttgagtgaaggctgctgagaggcctcagggcctggctgtcctg 720

Query: 751 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 810
|||
Sbjct: 721 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 780

Query: 811 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctcccttcaacctaaagagag 870
|||
Sbjct: 781 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctcccttcaacctaaagagag 840

Query: 871 ctgctccccaacagctggggcagttacttccgctacaatggctcgctcacaactccccct 930
|||
Sbjct: 841 ctgctccccaacagctggggcagttacttccgctacaatggctcgctcacaactccccct 900

Query: 931 tgctaccagagtgtgctctggacagttttttatagaagggtcccagatttcaatggaacag 990
|||
Sbjct: 901 tgctaccagagtgtgctctggacagttttttatagaagggtcccagatttcaatggaacag 960

Query: 991 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1050
|||
Sbjct: 961 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1020

Query: 1051 cagaactaccgagcccttcagcctctcaatcagcgcatgggtctttgcttctttcatcaa 1110
|||
Sbjct: 1021 cagaactaccgagcccttcagcctctcaatcagcgcatgggtctttgcttctttcatcaa 1080

Query: 1111 gcaggatcctcgtataccacaggtgaaatgctgagtctaggtgtaggaatcttggttggc 1170
|||
Sbjct: 1081 gcaggatcctcgtataccacaggtgaaatgctgagtctaggtgtaggaatcttggttggc 1140

Query: 1171 tgtctctgccttctcctggctgtttatttcatgtgtagaaagattcggaagaagaggctg 1230
|||
Sbjct: 1141 tgtctctgccttctcctggctgtttatttcatgtgtagaaagattcggaagaagaggctg 1200

Query: 1231 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1290
|||
Sbjct: 1201 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1260

Query: 1291 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1350
|||
Sbjct: 1261 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1320

Query: 1351 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1410
|||
Sbjct: 1321 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1380

Query: 1411 gacatctcttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1470
|||
Sbjct: 1381 gacatctcttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1440

Query: 1471 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgtgtttaatgcagaganca 1530

|||||
sbjct: 1441 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgtaatgcagagaaca 1500

Query: 1531 aactctgttttagttgcaggggaagtttgggatataaccccaaagtcctctaccccctcact 1590
|||||


sbjct: 1501 aactctgttttagttgcaggggaagtttgggatataaccccaaagtcctctaccccctcact 1560

Query: 1591 tttatggccctttccctagatataactgcgggatctctccttaggataaagagttgctgtt 1650
|||||

sbjct: 1561 tttatggccctttccctagatataactgcgggatctctccttaggataaagagttgctgtt 1620

Query: 1651 gaagttgtatatttttgatcaatatatttggaaattaaagtttctgacttt 1701
|||||

sbjct: 1621 gaagttgtatatttttgatcaatatatttggaaattaaagtttctgacttt 1671

>gi|19309420|emb|AL138795.21|  Human DNA sequence from clone RP4-790G17 on chromosome 1q21.1-
complete sequence
Length = 132823

Score = 948 bits (478), Expect = 0.0
Identities = 483/485 (99%)
Strand = Plus / Plus

Query: 1217 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 1276
|||||
sbjct: 78784 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 78843

Query: 1277 aggcataaattccttctcagataccatggatgtggatgacttcccttcatgcctatcagg 1336
|||||
sbjct: 78844 aggcataaattccttctcagataccatggatgtggatgacttcccttcatgcctatcagg 78903

Query: 1337 aagcctctaaaatggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 1396
|||||
sbjct: 78904 aagcctctaaaatggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 78963

Query: 1397 tcctccttcccttgacatctcttagagaggaatggaccaggtgtcattccaggaaga 1456
|||||
sbjct: 78964 tcctccttcccttgacatctcttagagaggaatggaccaggtgtcattccaggaaga 79023

Query: 1457 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 1516
|||||
sbjct: 79024 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 79083

Query: 1517 taatgcagagancaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 1576
|||||
sbjct: 79084 taatgcagagaacaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 79143

Query: 1577 tctaccccctcacttttatggccctttccctagatataactgcgggatctctccttaggat 1636
|||||
sbjct: 79144 tctaccccctcacttttatggccctttccctagatataactgcgggatctctccttaggat 79203

Query: 1637 aaagagttgctgttgaagttgtatatttttgatcaatatatttggaaattaaagtttctg 1696
|||||
sbjct: 79204 aaagagttgctgttgaagttgtatatttttgatcaatatatttggaaattaaagtttctg 79263

Query: 1697 acttt 1701
|||||
sbjct: 79264 acttt 79268

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Sbjct: 77231 agatcagaagacctcagtcctcccttcaacctaagagagctgctccccaacagctggg 77290

Query: 891 gcagtacttccgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctg 950
|||||
Sbjct: 77291 gcagtacttccgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctg 77350

Query: 951 gacagttttttatagaagggtcccagatttcaatggaacag 990
|||||
Sbjct: 77351 gacagttttttatagaagggtcccagatttcaatggaacag 77390

Score = 293 bits (148), Expect = 6e-76
Identities = 148/148 (100%)
Strand = Plus / Plus

Query: 522 cacagtgcactctctctgcccctctaccctgtatctgggtggacttccccgaaaatatgt 581
|||||
Sbjct: 76344 cacagtgcactctctctgcccctctaccctgtatctgggtggacttccccgaaaatatgt 76403

Query: 582 agctgcccagctccacctgcactggggtcagaaaggatccccaggggggtcagaacacca 641
|||||
Sbjct: 76404 agctgcccagctccacctgcactggggtcagaaaggatccccaggggggtcagaacacca 76463

Query: 642 gatcaacagtgaagccacatttgagag 669
|||||
Sbjct: 76464 gatcaacagtgaagccacatttgagag 76491

Score = 246 bits (124), Expect = 1e-61
Identities = 124/124 (100%)
Strand = Plus / Plus

Query: 988 cagctggaaaagcttcaggggacattgttctccacagaaggaggagccctctaagcttctg 1047
|||||
Sbjct: 77487 cagctggaaaagcttcaggggacattgttctccacagaaggaggagccctctaagcttctg 77546

Query: 1048 gtacagaactaccgagcccttcagcctctcaatcagcgcatgggtctttgcttctttcatc 1107
|||||
Sbjct: 77547 gtacagaactaccgagcccttcagcctctcaatcagcgcatgggtctttgcttctttcatc 77606

Query: 1108 caag 1111
|||||
Sbjct: 77607 caag 77610

Score = 198 bits (100), Expect = 3e-47
Identities = 100/100 (100%)
Strand = Plus / Plus

Query: 668 agctccacattgtacattatgactctgattcctatgacagcttgagtgaggctgctgaga 727
|||||
Sbjct: 76714 agctccacattgtacattatgactctgattcctatgacagcttgagtgaggctgctgaga 76773

Query: 728 ggcctcagggcctggctgtcctgggcatcctaattgaggt 767
|||||
Sbjct: 76774 ggcctcagggcctggctgtcctgggcatcctaattgaggt 76813

Score = 176 bits (89), Expect = 1e-40
 Identities = 89/89 (100%)
 Strand = Plus / Plus

Query: 1130 cagggtgaaatgctgagctctaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 1189
 |||||
 sbjct: 77982 cagggtgaaatgctgagctctaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 78041

Query: 1190 ctgtttatttcattgctagaaagattcgg 1218
 |||||
 sbjct: 78042 ctgtttatttcattgctagaaagattcgg 78070

Score = 137 bits (69), Expect = 9e-29
 Identities = 69/69 (100%)
 Strand = Plus / Plus

Query: 764 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatgaagtca 823
 |||||
 sbjct: 76993 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatgaagtca 77052


Query: 824 ggcataaag 832
 |||||
 sbjct: 77053 ggcataaag 77061

Score = 50.1 bits (25), Expect = 0.016
 Identities = 25/25 (100%)
 Strand = Plus / Plus

Query: 1110 agcaggatcctcgtataccacaggt 1134
 |||||
 sbjct: 77848 agcaggatcctcgtataccacaggt 77872

Score = 46.1 bits (23), Expect = 0.25
 Identities = 23/23 (100%)
 Strand = Plus / Plus

Query: 325 ggtcaacactggacgtatgaggg 347
 |||||
 sbjct: 74337 ggtcaacactggacgtatgaggg 74359

>[gi|28422259|gb|BC046995.1](#)  Mus musculus carbonic anhydrase 14, mRNA (cDNA clone MGC:54680 IMAGE:6491779), complete cds
 Length = 1654

Score = 805 bits (406), Expect = 0.0
 Identities = 844/990 (85%)
 Strand = Plus / Plus

Query: 270 tatgttggttctccgccctcctgctggaggtgatttggtatcctggctgcagatgggggtca 329
 |||||
 sbjct: 247 tatgttggttctcgtctcctgttaaaggtgacttggtatcctggctgcagatgggggtca 306

Query: 330 acactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtg 389
 |||||
 sbjct: 307 ccactggacatatgaaggccacacgggtcaggaccattggccaacctcttatcctgagtg 366

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7/26/04

Sbjct: 685 ctcccagtcctacagcagcttgagtgaggcagctcagaagccacagggcctggctgtcct 744

Query: 750 gggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtca 809

Sbjct: 745 aggcattcctcattgaggtgggcgagactgagaatccagcttatgatcacattctgagtcg 804

Query: 810 cttgcatgaagtcaggcataaagatcagaagacctcagtgccctcccttcaacctaaagaga 869

Sbjct: 805 tctacatgaaataagatacaaagatcagaagacctctgtgcctcccttcagcgtgagaga 864

Query: 870 gctgctccccaacacagctggggcagttacttccgctacaatggctcgctcacaaactcccc 929

Sbjct: 865 gctgttccccaacacagctggagcaattcttccgctacaacggctcactcacaaactcccc 924

Query: 930 ttgctaccagagtggtgctctggacagttttttatagaagggtcccagatttcaatggaaca 989

Sbjct: 925 ctgctaccagagtggtgctctggacagtttcaacagaagggcccagatttcaatgggaca 984

Query: 990 gctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggt 1049

Sbjct: 985 gttagagaagctccaggagacattgtcctctacagaagaggacccctctgagcccttgt 1044

Query: 1050 acagaactaccgagcccttcagcctctcaatcagcgcatgggtctttgcttctttcatcca 1109

Sbjct: 1045 acagaactacagagtccccagcctctcaaccagaggaccatctttgcttctttcatcca 1104

Query: 1110 agcaggatcctcgatataccacaggtgaaatgctgagttctaggtgtaggaatcttggttg 1169

Sbjct: 1105 agcaggaccactgtataccacaggagagatgctgggtctaggtgtgggaatcttggttg 1164

Query: 1170 ctgtctctgccttctcctggctgtttattttcattgctagaaagattcgggaagaagaggct 1229

Sbjct: 1165 atgtctttgccttctgctggctgtttattttcatcgctcaaaaaattaggaagaagcggct 1224

Query: 1230 ggaaaaccgaaagagtgtggtcttcacctc 1259

Sbjct: 1225 gggaaacaggaaaagtgtggttttcacctc 1254

>gi|6912284|ref|NP_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]
 gi|8928036|sp|Q9ULX7|CAHE_HUMAN carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)
 gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]
 gi|21706779|gb|AAH34412.1| carbonic anhydrase XIV, precursor [Homo sapiens]
 gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]
 Length = 337

Score = 682 bits (1760), Expect = 0.0
 Identities = 337/337 (100%), Positives = 337/337 (100%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
 Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
 Sbjct: 181 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG
 Sbjct: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]
 Length = 337

Score = 681 bits (1756), Expect = 0.0
 Identities = 336/337 (99%), Positives = 336/337 (99%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
 Sbjct: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
 Sbjct: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
 Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
 Sbjct: 181 LHEVRHKDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG
 Sbjct: 241 LEKLQGTFLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
 Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

|||||
 Sbjct: 1000 tatagaagggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080

|||||
 Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcattggtctttgcttctttcatccaagcaggatcctcgatataccacaggtgaaatg 1140

|||||
 Sbjct: 1120 cagcgcattggtctttgcttctttcatccaagcaggatcctcgatataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1200

|||||
 Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260

|||||
 Sbjct: 1240 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320

|||||
 Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatgggggtgtaggatctggccagaaacactgtag 1380

|||||
 Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatgggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttcccctggacatctcctagagaggaatggaccaggc 1440

|||||
 Sbjct: 1420 gagtagtaagcagatgtcctccttcccctggacatctcctagagaggaatggaccaggc 1479

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500

|||||
 Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaaactctgtttagttgcaggggaagtttggg 1560

|||||
 Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtttggg 1599

Query: 1561 atatacccccaggtcctctaccccctcacttttatggccctttccctagatatactgcgg 1620

|||||
 Sbjct: 1600 atatacccccaggtcctctaccccctcacttttatggccctttccctagatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1680

|||||
 Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701

|||||
 Sbjct: 1720 gaaattaaagtttctgacttt 1740

>gi|6009639|dbj|AB025904.1| **Luc** Homo sapiens mRNA for carbonic anhydrase 14, complete cds
 Length = 1757

Score = 3350 bits (1690), Expect = 0.0

Identities = 1698/1701 (99%)

Strand = Plus / Plus

7/26/04

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|||||
sbjct: 880 acctcagtgccctcccttcaacctaagagagctgctccccaacagctggggcagtacttc 939

Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960
sbjct: 940 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 999

Query: 961 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020
sbjct: 1000 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080
sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcatggctcttcttcttcatccaagcaggatcctcgataccacaggtgaaatg 1140
sbjct: 1120 cagcgcatggctcttcttcttcatccaagcaggatcctcgataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1200
sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgctgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260
sbjct: 1240 attgctagaaagattcggagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320
sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380
sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1440
sbjct: 1420 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1479

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500
sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgtttagttgcaggggaagtttggg 1560
sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtttggg 1599

Query: 1561 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1620
sbjct: 1600 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1680
sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701
sbjct: 1720 gaaattaaagtttctgacttt 1740
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